

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne  
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
(B) STREET: 1100 New York Ave., Suite 600  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1442 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 15..1139

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC  
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys  
1 5 10

50

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AAT Asn	GGC Gly	GCA Ala 15	ATC Ile	TCA Ser	GCT Ala	CAC His	CGC Arg 20	AAC Asn	CTC Leu	CGC Arg	CTC Leu	CCG Pro 25	GGT Gly	TCA Ser	AGC Ser	98
GAT Asp 30	TCT Ser	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser 35	CCA Pro	GTA Val	GCT Ala	GGG Gly	ATT Ile 40	ACA Thr	GGC Gly	ATG Met	TGC Cys	146
ACC Thr 45	CAC His	GCT Ala	CGG Arg	CTA Leu	ATT Ile 50	TTG Leu	TAT Tyr	TTT Phe	TTT Phe	TTA Leu 55	GTA Val	GAG Glu	ATG Met	GAG Glu	TTT Phe 60	194
CTC Leu	CAT His	GTT Val	GGT Gly	CAG Gln 65	GCT Ala	GGT Gly	CTC Leu	GAA Glu	CTC Leu 70	CCG Pro	ACC Thr	TCA Ser	GAT Asp 75	GAT Asp 75	CCC Pro	242
TCC Ser	GTC Val	TCG Ser	GCC Ser 80	TCC Ser	CAA Gln	AGT Ser	GCT Ala	AGA Arg 85	TAC Tyr	AGG Arg	ACT Thr	GGC Gly	CAC His 90	CAT His	GCC Ala	290
CGG Arg	CTC Leu	TGC Cys 95	CTG Leu	GCT Ala	AAT Asn	TTT Phe	TGT Cys 100	GGT Gly	AGA Arg	AAC Asn	AGG Arg 105	GTT Val	CTG Ser	ATG Leu	ATG Met	338
TGC Cys 110	CCA Pro	AGC Ser	TGG Trp	TCT Ser	CCT Pro	GAG Glu 115	CTC Leu	AAG Lys	CAG Gln	TCC Ser	ACC Thr 120	TGC Cys	CTC Leu	AGC Ser	CTC Leu	386
CCA Pro 125	AAG Lys	TGC Cys	TGG Trp	GAT Asp 130	TAC Arg	AGG Arg	CGT Arg	GCA Ala	GTG Val 135	CCT Pro	GGC Gly	CTT Leu	TTT Phe 140	ATT Ile		434
TTA Leu	TTT Phe	TTT Phe	TTA Leu	AGA Arg 145	CAC His	AGG Arg	TGT Cys	CCC Pro	ACT Thr 150	CTT Leu	ACC Thr	CAG Gln	GAT Asp 155	GAA Glu 155	GTG Val	482
CAG Gln	TGG Trp	TGT Cys 160	GAT Asp	CAC His	AGC Ser	TCA Ser	CTG Leu	CAG Gln 165	CCT Pro	TCA Ser	ACT Thr	CCT Pro	GAG Glu 170	ATC Ile	AAG Lys	530
CAT His	CCT Pro	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CAA Gln 180	GTA Val	GCT Ala	GGG Gly	ACC Thr	AAA Lys 185	GAC Asp	ATG Met	CAC His	578
CAC His	TAC Tyr 190	ACC Thr	TGG Trp	CTA Leu	ATT Ile	TTT Phe 195	ATT Ile	TTT Phe	ATT Ile	TTT Phe	AAT Asn 200	TTT Phe	TTG Leu	AGA Arg	CAG Gln	626
AGT Ser 205	CTC Leu	AAC Asn	TCT Ser	GTC Val	ACC Thr 210	CAG Gln	GCT Ala	GGA Gly	GTG Val	CAG Val 215	TGG Trp	CGC Arg	AAT Asn	CTT Leu	GGC Gly 220	674
TCA Ser	CTG Leu	CAA Gln	CCT Pro	CTG Leu 225	CCT Pro	CCC Pro	GGG Gly	TTC Phe	AAG Lys 230	TTA Leu	TTC Phe	TCC Ser	TGC Cys	CCC Pro 235	AGC Ser	722
CTC Leu	CTG Leu	AGT Ser	AGC Ser	TGG Trp 240	GAC Asp	TAC Tyr	AGG Arg	CGC Arg	CCA Pro 245	CCA Pro	CGC Arg	CTA Leu	GCT Ala 250	AAT Asn	TTT Phe	770
TTT Phe	GTA Val 255	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GGG Gly 260	TTC Phe	ACC Thr	ATG Met	TTC Phe	GCC Ala 265	AGG Arg	TTG Leu	ATC Ile	818
TTG ATC	ATC TCT	GGA CCT	TGT GAT	CTG CTC	CCT GCC	TGC GCC	TCC CAA	AGT GCT								866

Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala	
270 275 280	
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT	914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	
285 290 295 300	
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG	962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	
305 310 315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC	1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	
320 325 330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA	1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	
335 340 345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT	1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	
350 355 360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT	1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	
365 370 375	
TCCAAAGTGC TGGGATTACA GGC GTGAGCC ACCTCACC CA GCCGCTAAT TTAGATAAAA	1219
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAAA CTCTGGCTT	1279
CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTTA AACAGTTACA	1339
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	1399
GTAACAGAGT TCTTTTATAA CTTTAAACA AAGCTTTAGA GCA	1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile	
1 5 10 15	
Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala	
20 25 30	
Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg	
35 40 45	
Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly	
50 55 60	
Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala	
65 70 75 80	
Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu	

09961467.092601

85										90					95				
Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp				
			100						105						110				
Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	Pro	Lys	Cys	Trp				
		115					120						125						
Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	Leu	Phe	Phe	Leu				
	130					135					140								
Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	Gln	Trp	Cys	Asp				
	145				150						155				160				
His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala				
				165					170					175					
Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp				
			180					185					190						
Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser				
		195					200						205						
Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro				
	210					215					220								
Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser				
	225				230						235				240				
Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu				
				245					250					255					
Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly				
		260						265					270						
Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly				
		275					280						285						
Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met				
		290				295					300								
Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly				
	305				310						315				320				
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser				
			325						330					335					
Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn				
			340				345						350						
Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp				
		355				360						365							
Ser	Gln	Thr	Pro	Asp	Leu	Arg													
		370				375													

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1381 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCGAG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC GCACAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGCCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA	180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC	300
TGCCGTGGCTA ATTTTGTGG TAGAAACAGS GTTTCACCTG TGTGCGCCAA GCTGGTCTCC	360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC	420
GTGCTGGCC TTTTATTTTT ATTTTMTTTA AGACACAGGT GTACCACTCT TACCCAGGAT	480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC	540
TCCTGCCCTA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT	600
TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCAG GCTGGAGTGC	660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCTCCCGG GTTCAAGTTA TTCTCTGTCC	720
CCAGCTCCTC GAGTAGCTGG GACTACAGGC GCCCACCAGC CCTAGCTAAT TTTTMTGTAT	780
TTTTAGTAGA GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTTGATCTC TTGACCTTGT	840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCTGTACT CCACGCCGGC	900
CTATTTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC	960
AATGGCAAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC	1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT	1080
CATTAGAGGC GGGTTTACCA TATTGTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA	1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC	1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
TCAAACCTCT GGCCTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA	1380
C	1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

**060945** = **060903**

**060948** **U.S.**

[illegible][illegible][illegible]

**060948** **U.S.**

062801-062803

24

(2) INFORMATION FOR SEQ ID NO:8:

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

(2) INFORMATION FOR SEQ ID NO:8:

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

- (ii) MOLECULE TYPE: cDNA

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09964667.092801



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

096467.092801